

CLAIMS

What is claimed is:

1. A method of screening a compound to determine whether the compound binds to a harA polypeptide, which comprises: contacting the harA polypeptide with the compound under conditions suitable for binding; and detecting whether the compound binds to the harA polypeptide, wherein the harA polypeptide comprises an amino acid sequence at least 75% identical to (a) the amino acid sequence shown in Figure 2 (SEQ ID NO:2) or (b) the amino acid sequence shown in Figure 4 (SEQ ID NO:4).  
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2. A method of screening a compound to determine whether the compound inhibits harA activity, which comprises: measuring the activity of a harA polypeptide (i) in the absence and (ii) in the presence of the compound, under conditions suitable for measuring harA activity; wherein a decrease in harA activity in the presence of the compound compared to the harA activity in the absence of the compound identifies the compound as inhibiting harA activity, wherein the harA polypeptide comprises an amino acid sequence at 10 least 75% identical to (a) the amino acid sequence shown in Figure 2 (SEQ ID NO:2) or (b) the amino acid sequence shown in Figure 4 (SEQ ID NO:4).  
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3. The method of claim 2, wherein the harA activity measured is NTPase activity.
4. The use of a hygromycin A-resistant strain of *E. faecalis* or *B. subtilis* to determine whether an antibacterial agent is effective in treating organisms which exhibit harA-mediated drug resistance.  
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5. The use of a nucleic acid encoding a harA polypeptide to identify an organism containing a harA gene, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:  
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  - (a) a nucleotide sequence which is at least 75% identical to (i) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) or (ii) the nucleotide sequence shown in Figure 3 (SEQ ID NO:3);
  - (b) a nucleotide sequence complementary to the nucleotide sequence of (a); and
  - (c) a nucleotide sequence that is degenerate to the nucleotide sequence of (a) or (b).
6. A recombinant vector comprising a nucleic acid encoding a harA polypeptide, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:  
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  - (a) a nucleotide sequence which is at least 75% identical to (i) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) or (ii) the nucleotide sequence shown in Figure 3 (SEQ ID NO:3);
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  - (a) a nucleotide sequence which is at least 75% identical to (i) the nucleotide sequence shown in Figure 1 (SEQ ID NO:1) or (ii) the nucleotide sequence shown in Figure 3 (SEQ ID NO:3);

(b) a nucleotide sequence complementary to the nucleotide sequence of (a);  
and

(c) a nucleotide sequence that is degenerate to the nucleotide sequence of (a) or (b).

5 7. A cell comprising the vector of claim 6.

8. A vector of claim 6 selected from pMP, pJPM1, pGEM-T, pVA891, pSK<sup>-</sup>, pUC8, pUC9, pBR322, pBR329, pPL, pKK223 and pQE50.

9. A cell comprising the vector of claim 8.

10. A vector of claim 6 which is pMP-bac-A1-1 (ATCC Accession No. PTA-2552) or pGEM-T/harA (ATCC Accession No. PTA-2552).

10 2551) or pGEM-T/harA (ATCC Accession No. PTA-2552).

11. A cell comprising the vector of claim 10.

12. A recombinant vector comprising nucleic acid encoding a harA polypeptide, wherein the nucleic acid encoding the harA polypeptide comprises a nucleotide sequence comprising a chloramphenicol resistance insertion or an erythromycin resistance insertion.

15 13. A cell comprising the vector of claim 12.

14. The cell of claim 13 which is the *Bacillus subtilis* strain JH642 *expZ::CAT* (ATCC Accession No. PTA-2480) or the *Enterococcus faecalis* strain OG1X *harA::ERM* (ATCC Accession No. PTA-2550).

15. A recombinant harA polypeptide comprising an amino acid sequence which  
20 is at least 75% identical to (i) the amino acid sequence shown in Figure 2 (SEQ ID NO:2) or  
(ii) the amino acid sequence shown in Figure 4 (SEQ ID NO:4).

16. An immunological composition comprising the harA polypeptide of claim 15 and a pharmaceutically acceptable carrier.

17. An immunological composition of claim 16, which further comprises an  
25 adjuvant.